

Fig. 1

1B

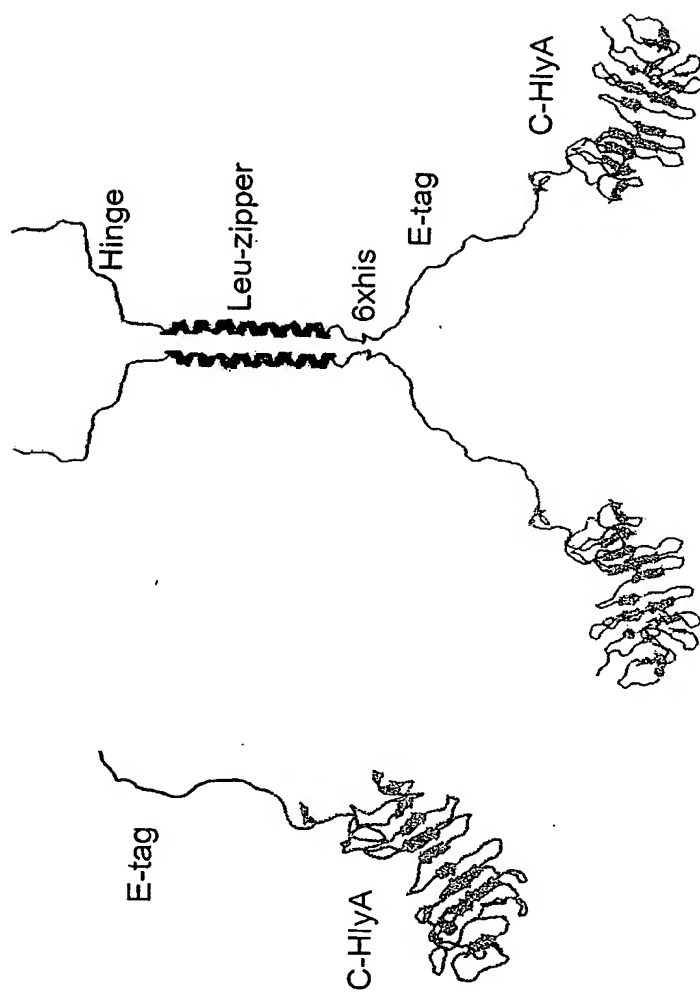


Fig. 1 (cont.)

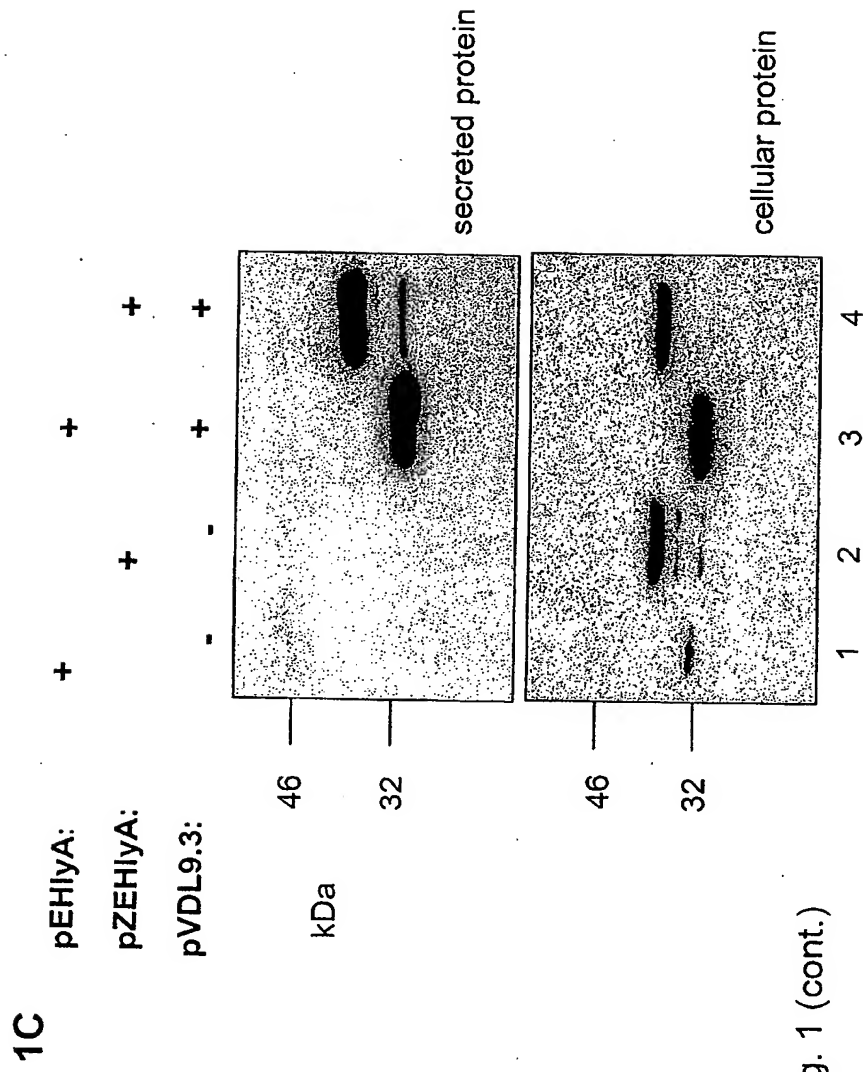


Fig. 1 (cont.)

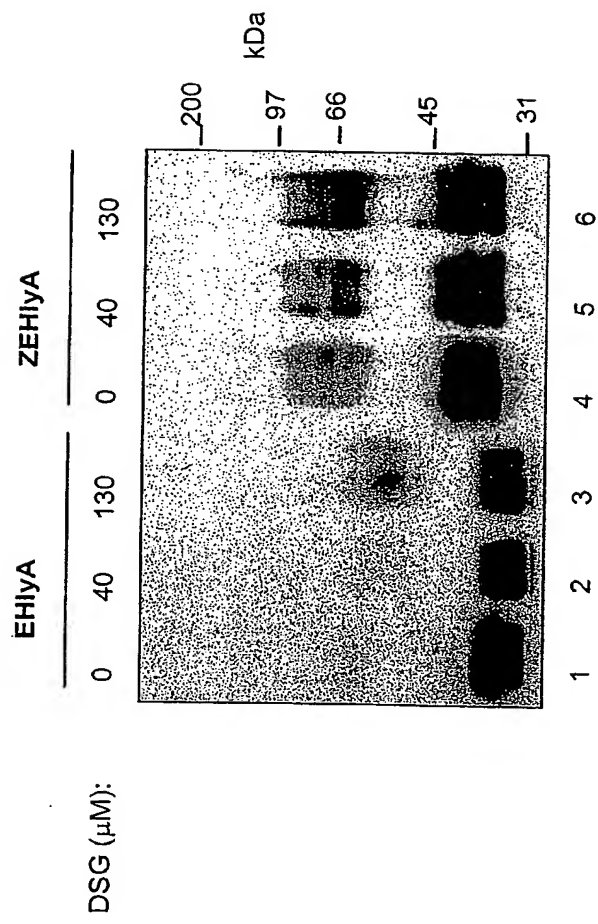


Fig. 2

3A

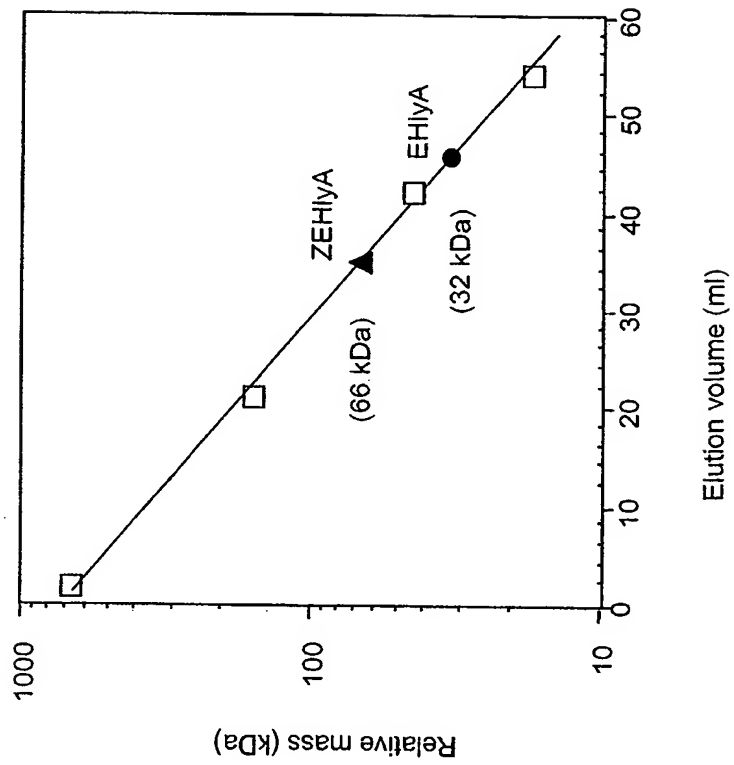
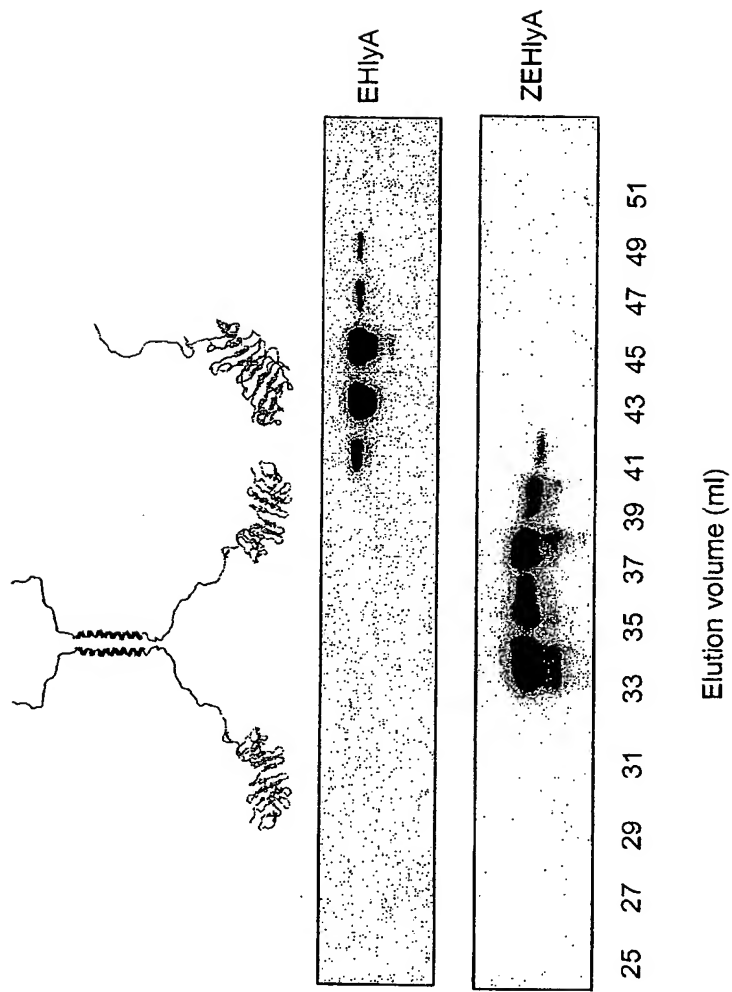


Fig. 3

3B

Fig. 3 (cont.)



4A



4B

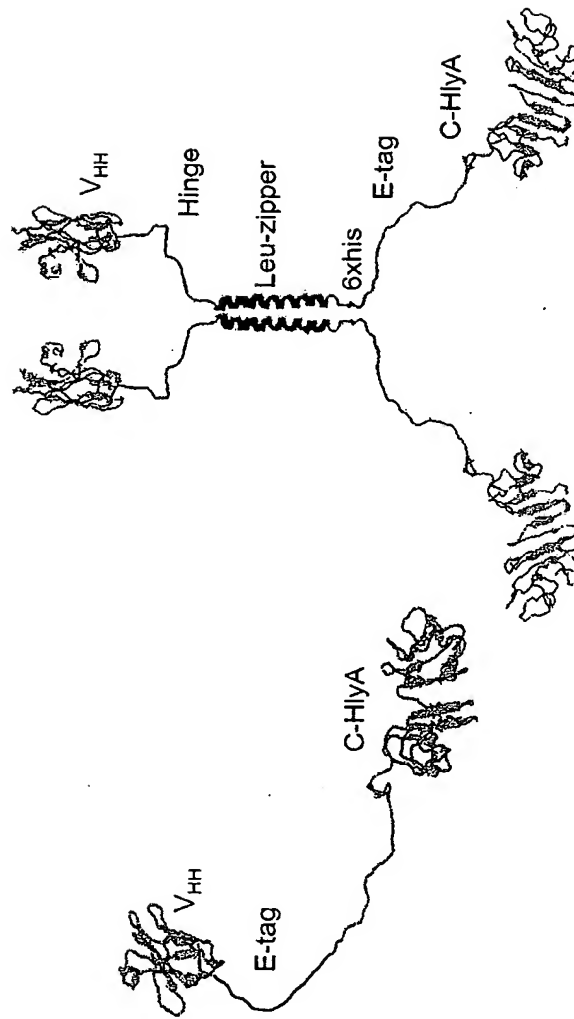


Fig. 4

4C

4D

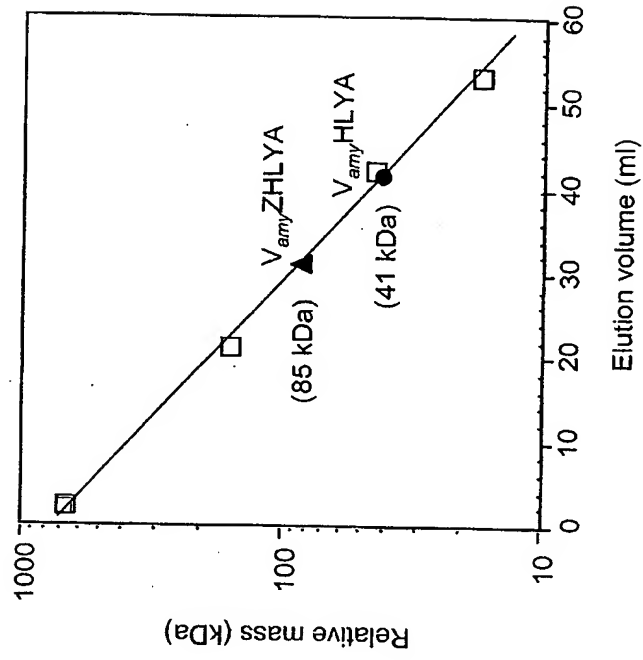
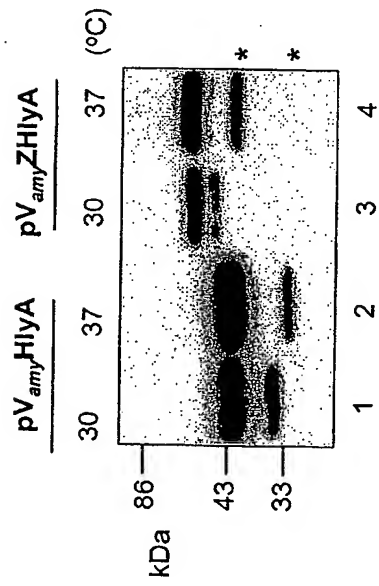
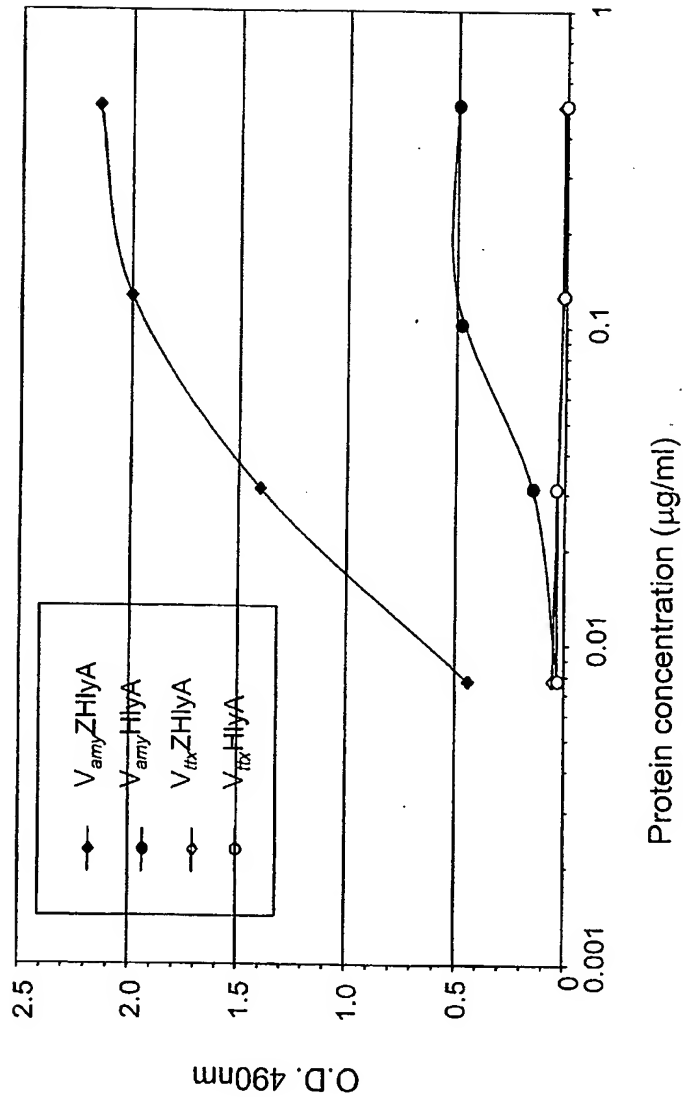


Fig. 4 (cont.)

Fig. 5



pZEHlyA map

AGCGGATAACAATTCACACAGGAAACAGCT (sequence before the ATG)

Fig. 6

```

GGTAATGACAAGTTGTACGGCAGTGAGGGAGCAGACCTGCTTGATGGCGGAGAAGGGAAT
301 -----+-----+-----+-----+-----+ 360
CCATTACTGTTCAACATGCCGTCACCTCCCTCGTCTGGACGAACTACCGCCTCTTCCCTTA

a   G N D K L Y G S E G A D L L D G G E G N -

GATCTTCTGAAAGGTGGATATGGTAATGATATTTATCGTTATCTTTCAGGATATGGCCAT
361 -----+-----+-----+-----+-----+ 420
CTAGAAGACTTTCCACCTATACCATTACTATAAATAGCAATAGAAAGTCTATACCGGTA

a   D L L K G G Y G N D I Y R Y L S G Y G H -

CATATTATTGACGATGAAGGGGGAAAGACGATAAACTCAGTTTAGCTGATATAGATTTTC
421 -----+-----+-----+-----+-----+ 480
GTATAATAACTGCTACTTCCCCCTTTCTGCTATTTGAGTCAAATCGACTATATCTAAAG

a   H I I D D E G G K D D K L S L A D I D F -

CGGGACGTTGCCTTTAAGCGAGAAGGGAATGACCTCATTATGTATAAAGCTGAAGGTAAT
481 -----+-----+-----+-----+-----+ 540
GCCCTGCAACGGAAATTCGCTCTTCCCTTACTGGAGTAATACATATTTGACTTCCATTA

a   R D V A F K R E G N D L I M Y K A E G N -

GTTCTTTCTATTGGCCACAAAAATGGTATTACATTTAAAACTGGTTTGAAAAAGAGTCA
541 -----+-----+-----+-----+-----+ 600
CAAGAAAGATAACCGGTGTTTTTACCATAATGTAAATTTTTGACCAAACCTTTTCTCAGT

a   V L S I G H K N G I T F K N W F E K E S -

GATGATCTCTCTAATCATCAGATAGAGCAGATTTTTGATAAAGACGGCAGGGTAATCACA
601 -----+-----+-----+-----+-----+ 660
CTACTAGAGAGATTAGTAGTCTATCTCGTCTAAAACTATTTCTGCCGTCCCATTAGTGT

a   D D L S N H Q I E Q I F D K D G R V I T -

CCAGATTCTCTTAAAAAAGCATTTTGAATATCAGCAGAGTAATAACAAGGTAAGTTATGTG
661 -----+-----+-----+-----+-----+ 720
GGTCTAAGAGAATTTTTTCGTAAACTTATAGTCGTCTCATTATTGTTCCATTCAATACAC

a   P D S L K K A F E Y Q Q S N N K V S Y V -

TATGGACATGATGCATCAACTTATGGGAGCCAGGACAATCTTAATCCATTAATTAATGAA
721 -----+-----+-----+-----+-----+ 780
ATACCTGTACTACGTAGTTGAATACCCTCGGTCTGTAGTAATTAGGTAATTAATTACTT

a   Y G H D A S T Y G S Q D N L N P L I N E -

```

Fig. 6 (cont.)

PstI
|

781 ATCAGCAAAATCATTTCAGCTGCAGGTAACCTCGATGTTAAGGAGGAAAGATCTGCCGCT
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 840
TAGTCGTTTTAGTAAAGTCGACGTCCATTGAAGCTACAATTCCTCCTTTCTAGACGGCGA

a I S K I I S A A G N F D V K E E R S A A -

NdeI
|

841 TCTTTATTGCAGTTGTCCGGTAATGCCAGTGATTTTTCATATGGACGGAACCTCAATAACT
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 900
AGAAATAACGTCAACAGGCCATTACGGTCACTAAAAAGTATACCTGCCTTGAGTTATTGA

a S L L Q L S G N A S D F S Y G R N S I T -

TTGACAGCATCAGCATAA

901 -----+----- 918
AACTGTCGTAGTCGTATT

a L T A S A * -

Cutting enzymes:

AccI	BamHI	EcoRI	HindIII	NdeI	PstI	SacI	SalI
SmaI	XbaI						

Not cutting enzymes:

KpnI	NcoI	NheI	NotI	SacII	SphI
------	------	------	------	-------	------

Fig. 6 (cont.)

pZEHLIA2SD map

With 11 restriction enzymes: ECORI BGLII BAMHI NCOI NHEI SFII SALI XMAI
XBAI EAGI SALI HINDIII

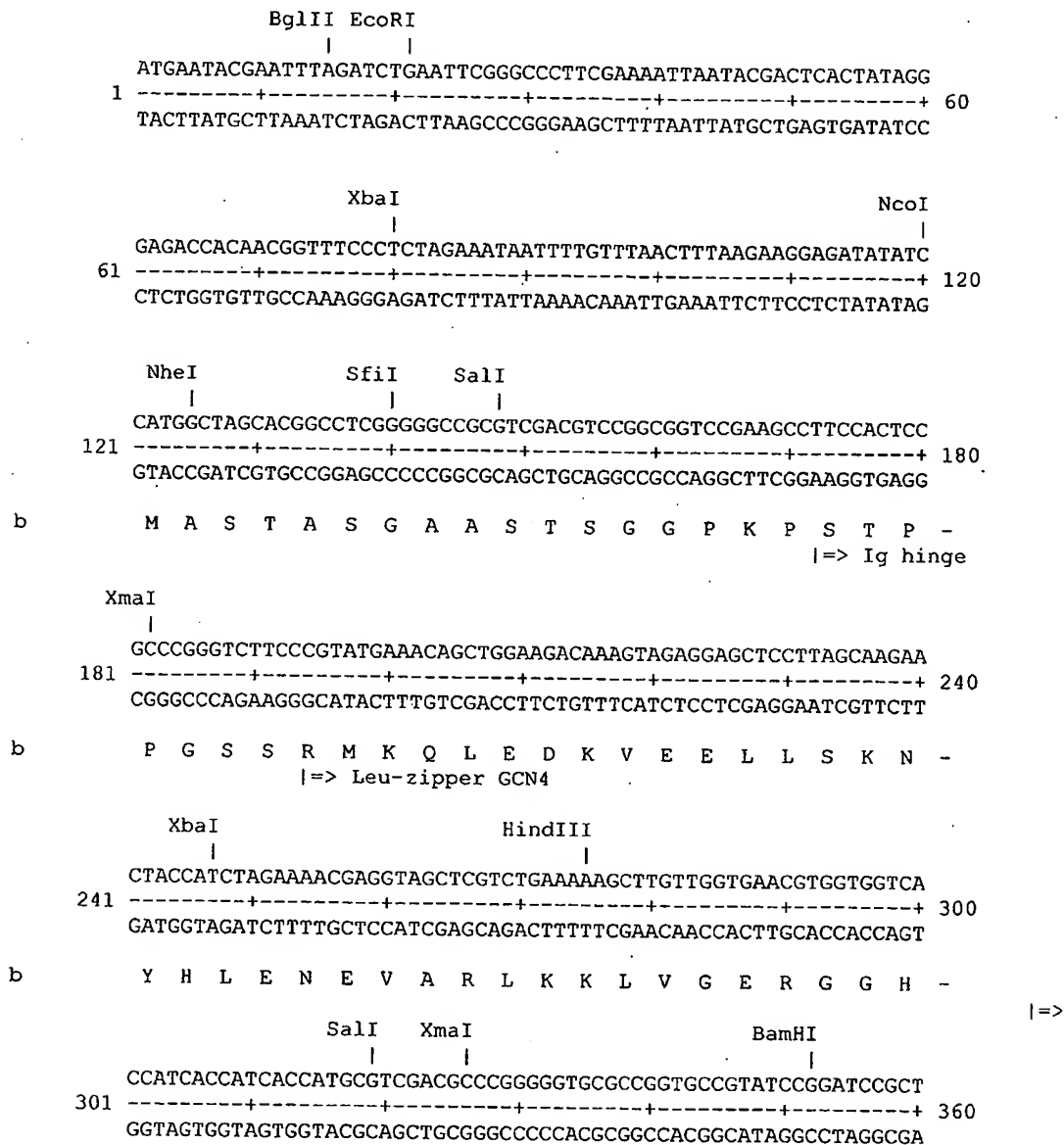


Fig. 7

b H H H H H A S T P G G A P V P Y P D P L -
 6xhis tag | => E-tag
 EagI
 |
 361 -----+-----+-----+-----+-----+ 420
 GGAACCGGCCGGGGAAAATTCTCTTGCTAAAAATGTATTATCCGGTGGAAAAGGTAATGA
 CCTTGGCCGGCCCTTTTAAGAGAACGATTTTACATAATAGCCACCTTTTCCATTACT

b E P A G E N S L A K N V L S G G K G N D -
 | => C-hlyA
 421 -----+-----+-----+-----+-----+ 480
 CAAGTTGTACGGCAGTGAGGGAGCAGACCTGCTTGATGGCGGAGAAGGGAATGATCTTCT
 GTTCAACATGCCGTCACTCCCTCGTCTGGACGAACCTACGCCTCTTCCCTTACTAGAAGA

b K L Y G S E G A D L L D G G E G N D L L -
 481 -----+-----+-----+-----+-----+ 540
 GAAAGGTGGATATGGTAATGATATTTATCGTTATCTTTCAGGATATGGCCATCATATTAT
 CTTTCACCTATACCATTACTATAAATAGCAATAGAAAGTCCTATACGGTAGTATAATA

b K G G Y G N D I Y R Y L S G Y G H H I I -
 541 -----+-----+-----+-----+-----+ 600
 TGACGATGAAGGGGGGAAAGACGATAAACTCAGTTTAGCTGATATAGATTTCCGGGACGT
 ACTGCTACTTCCCCCTTTCTGCTATTTGAGTCAAATCGACTATATCTAAAGGCCCTGCA

b D D E G G K D D K L S L A D I D F R D V -
 601 -----+-----+-----+-----+-----+ 660
 TGCCTTTAAGCGAGAAGGGAATGACCTCATTATGTATAAAGCTGAAGGTAATGTTCTTTC
 ACGGAAATTCGCTCTTCCCTTACTGGAGTAATACATATTTGACTTCCATTACAAGAAAG

b A F K R E G N D L I M Y K A E G N V L S -
 661 -----+-----+-----+-----+-----+ 720
 TATTGGCCACAAAAATGGTATTACATTAAAAACTGGTTTGAAAAAGAGTCAGATGATCT
 ATAACCGGTGTTTTTACCATAATGTAAATTTTGACCAAACCTTTTCTCAGTCTACTAGA

b I G H K N G I T F K N W F E K E S D D L -
 721 -----+-----+-----+-----+-----+ 780
 CTCTAATCATCAGATAGAGCAGATTTTGTATAAAGACGGCAGGGTAATCACACCAGATTC
 GAGATTAGTAGTCTATCTCGTCTAAAACTATTTCTGCCGTCCCATAGTGTGGTCTAAG

b S N H Q I E Q I F D K D G R V I T P D S -
 781 -----+-----+-----+-----+-----+ 840
 TCTTAAAAAGCATTTGAATATCAGCAGAGTAATAACAAGGTAAGTTATGTGTATGGACA
 AGAATTTTTTCGTAAACTTATAGTCGTCTCATTATTGTTCCATTCAATACACATACCTGT

Fig. 7 (cont.)

b L K K A F E Y Q Q S N N K V S Y V Y G H -
 TGATGCATCAACTTATGGGAGCCAGGACAATCTTAATCCATTAATTAATGAAATCAGCAA
 841 -----+-----+-----+-----+-----+ 900
 ACTACGTAGTTGAATACCCTCGGTCCTGTTAGAATTAGGTAATTAATTACTTTAGTCGTT

b D A S T Y G S Q D N L N P L I N E I S K -
 BglII
 |
 AATCATTTCAGCTGCAGGTAACCTTCGATGTTAAGGAGGAAAGATCTGCCGCTTCTTTATT
 901 -----+-----+-----+-----+-----+ 960
 TTAGTAAAGTCGACGTCCATTGAAGCTACAATTCCTCCTTTCTAGACGGCGAAGAAATAA

b I I S A A G N F D V K E E R S A A S L L -
 GCAGTTGTCCGTAATGCCAGTGATTTTTCATATGGACGGAACCTCAATAACTTTGACAGC
 961 -----+-----+-----+-----+-----+ 1020
 CGTCAACAGGCCATTACGGTCACTAAAAAGTATACCTGCCTTGAGTTATTGAAACTGTGC

b Q L S G N A S D F S Y G R N S I T L T A -
 ATCAGCATAATATATTAATTTAAATGATAGCAATCTTACTGGGCTGTGCCACATAAGATT
 1021 -----+-----+-----+-----+-----+ 1080
 TAGTCGTATTATATAATTAAATTTACTATCGTTAGAATGACCCGACACGGTGTATTCTAA

b S A * -
 GCTATTTTTTTGGAGTCATAATGGATTCTTGTCAAAAATTGATTATGGGTATACGCCC
 1081 -----+-----+-----+-----+-----+ 1140
 CGATAAAAAAACCTCAGTATTACCTAAGAACAGTATTTTAACTAATACCCAATATGCGGG

1141 TGGAGATTTTAGCCCAATACCATAACGTCTCTGTTAACCCGGAAGAAATTAAACATAGAT
 -----+-----+-----+-----+-----+ 1200
 ACCTCTAAATCGGGTTATGGTATTGCAGAGACAATTGGGCCTTCTTTAATTTGTATCTA

1201 TTGACACAGACGGGACTGGTCTGGGATTAACGTCATGGTTGCTTGCTGCGAAATCTTTAG
 -----+-----+-----+-----+-----+ 1260
 AACTGTGTCTGCCCTGACCAGACCCTAATTGCAGTACCAACGAACGACGCTTTAGAAATC

1261 AACTAAAGGTAAACAGGTAAAAAACAATTGACCGATTAAACTTTATTTCTCTGCCCG
 -----+-----+-----+-----+-----+ 1320
 TTGATTTCCATTTTGTCCATTTTTTTTGTAACTGGCTAATTTGAAATAAGAGACGGGC

1321 CATTAGTCTGGAGAGAGGATGGACGTCATTTTATTCTGACTAAAGTCAGTAAAGAAGCAA
 -----+-----+-----+-----+-----+ 1380
 GTAATCAGACCTCTCTCCTACCTGCAGTAAAATAAGACTGATTTTCAGTCATTTCTTCGTT

Fig. 7 (cont.)

```

ACAGATATCTTATTTCTGATCTGGAGCAGCGAAATCCCGTGTTCTCGAACAGTCTGAGT
1381 -----+-----+-----+-----+-----+ 1440
TGTC'TATAGAAATAAAGACTAGACCTCGTCGCTTTAGGGGCACAAGAGCTTGTCAGACTCA

TTGAGGCGTTATATCAGGGGCATATTATTCTTATCGCTTCCCGTTCTTCTGTTGCCGGGA
1441 -----+-----+-----+-----+-----+ 1500
AACTCCGCAATATAGTCCCGGTATAATAAGAATAGCGAAGGGCAAGAAGACAACGGCCCT

AACTGGCGAAATTTGACTTTACCTGGTTTATTCCTGCCATTATAAAATACAGGAGAATAT
1501 -----+-----+-----+-----+-----+ 1560
TTGACCGCTTTAAACTGAAATGGACCAAATAAGGACGTAATATTTTATGTCCTCTTATA

TTATTGAAACCCTTGTTGTGTCTGTTTTTTTACAATTATTTGCATTAATAACCCCTTTT
1561 -----+-----+-----+-----+-----+ 1620
AATAACTTTGGGAACAACACAGACAAAAAATGTTAATAAACGTAATTATTGGGGGGAAA

TTTTTCAGGTGGTTATGGACAAAGTATTAGTGCACAGGGGATTTTCAACTCTTAATGTTA
1621 -----+-----+-----+-----+-----+ 1680
AAAAAGTCCACCAATACCTGTTTCATAATCACGTGTCCCTAAAAGTTGAGAATTACAAT

TTACTGTGCGATTATCTGTTGTGGTGGTGGTTGAGATTATACTCAGCGGTTTAAGAACTT
1681 -----+-----+-----+-----+-----+ 1740
AATGACAGCGTAATAGACAACACCACCACAACTCTAATATGAGTCGCCAAATCTTGAA

ACATTTTTGCACATAGTACAAGTCGGATTGATGTTGAGTTGGGTGCCAAACTCTTCCGGC
1741 -----+-----+-----+-----+-----+ 1800
TGTA AAAACGTGTATCATGTT CAGCCTAACTACA ACTCAACCCACGTTTGAGAAGGCCG

ATTACTGGCGCTACCGATCTCTTATTTTGAGAGTCGTCGTGTTGGTGATACTGTTGCCA
1801 -----+-----+-----+-----+-----+ 1860
TAAATGACCGCGATGGCTAGAGAATAAACTCTCAGCAGCACAACTATGACAACGGT

GGGTAAGAGAATTAGACCAGATCCGTAATTTTCTGACAGGACAGGCATTAACATCTGTTCT
1861 -----+-----+-----+-----+-----+ 1920
CCCATTCTCTTAATCTGGTCTAGGCATTAAAGACTGTCCTGTCCGTAATTGTAGACAAG

                                     HindIII
                                     |
TGGACTTATTATTTTCATTCATATTTTTCGCGTAATGTGGTATTACAGTCCAAAGCTT
1921 -----+-----+-----+-----+-----+ 1979
ACCTGAATAATAAAAGTAAGTATAAAAAACGCCATTACACCATAATGTCAGGTTTCGAA

```

Fig. 7 (cont.)

Cutting enzymes:

BamHI	BglII	EagI	EcoRI	HindIII	NcoI	NheI	SalI
SfiI	XbaI	XmaI					

Not cutting enzymes:

None

Fig. 7 (cont.)

pVamyHLYA map

With 8 enzymes: NCOI PSTI SALI HINDIII SFII BAMHI NOTI ECORI PSTI

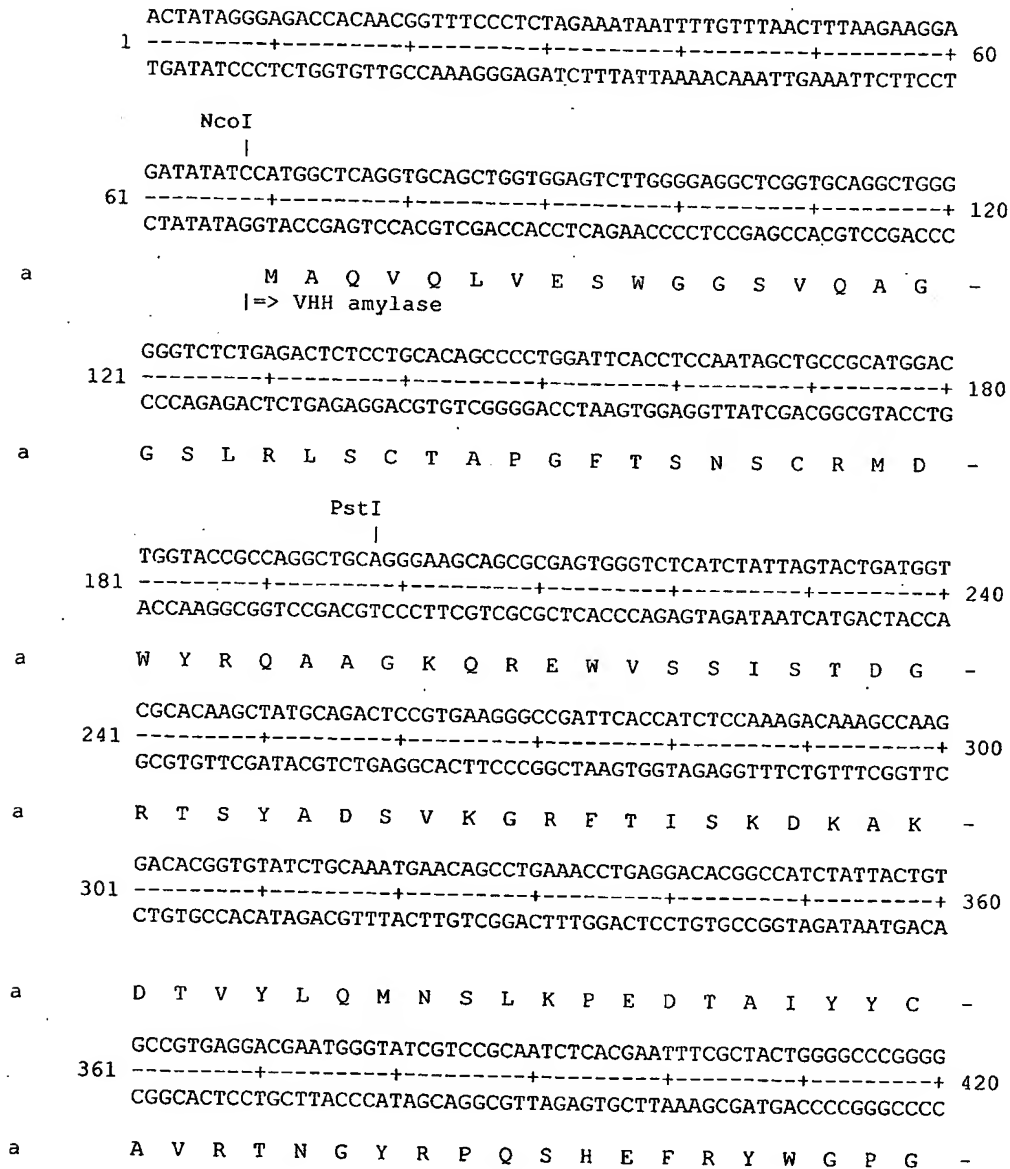


Fig. 8

Fig. 8 (cont.)

```

a      R V I T P D S L K K A F E Y Q Q S N N K -
      GTAAGTTATGTGTATGGACATGATGCATCAACTTATGGGAGCCAGGACAATCTTAATCCA
961  -----+-----+-----+-----+-----+-----+-----+ 1020
      CATTCAATACACATACCTGTACTACGTAGTTGAATACCCTCGGTCCTGTTAGAATTAGGT

a      V S Y V Y G H D A S T Y G S Q D N L N P -
                                PstI
                                |
      TTAATTAATGAAATCAGCAAAATCATTTCAGCTGCAGGTAACCTTCGATGTTAAGGAGGAA
1021  -----+-----+-----+-----+-----+-----+-----+ 1080
      AATTAATTACTTTAGTCGTTTTAGTAAAGTCGACGTCCATTGAAGCTACAATTCCTCCTT

a      L I N E I S K I I S A A G N F D V K E E -
      AGATCTGCCGCTTCTTTATTGCAGTTGTCCGTAATGCCAGTGATTTTTTCATATGGACGG
1081  -----+-----+-----+-----+-----+-----+-----+ 1140
      TCTAGACGGCGAAGAAATAACGTCAACAGGCCATTACGGTCACTAAAAAGTATACCTGCC

a      R S A A S L L Q L S G N A S D F S Y G R -
      AACTCAATAACTTTGACAGCATCAGCATAATATATTAATTTAAATGATAGCAATCTTACT
1141  -----+-----+-----+-----+-----+-----+-----+ 1200
      TTGAGTTATTGAAACTGTCGTAGTCGTATTATATAATTAATTTACTATCGTTAGAATGA

a      N S I T L T A S A * -
      GGGCTGTGCCACATAAGATTGCTATTTTTTTGGAGTCATAATGGATTCTTGTCATAAAAT
1201  -----+-----+-----+-----+-----+-----+-----+ 1260
      CCCGACACGGTGTATTCTAACGATAAAAAAACCTCAGTATTACCTAAGAACAGTATTTTA

      TGATTATGGGTATACGCCCTGGAGATTTAGCCCAATACCATAACGTCTCTGTAAACCC
1261  -----+-----+-----+-----+-----+-----+-----+ 1320
      ACTAATACCCAATATGCGGGACCTCTAAATCGGGTTATGGTATTGCAGAGACAATTGGG

      GGAAGAAATTAAACATAGATTTGACACAGACGGGACTGGTCTGGGATTAACGTCATGGTT
1321  -----+-----+-----+-----+-----+-----+-----+ 1380
      CCTTCTTTAATTTGTATCTAAACTGTGTCTGCCCTGACCAGACCCTAATTGCAGTACCAA

      GCTTGCTGCGAAATCTTTAGAACTAAAGGTAAACAGGTAAAAAAACAATTGACCGATT
1381  -----+-----+-----+-----+-----+-----+-----+ 1440
      CGAACGACGCTTTAGAAATCTTGATTCCATTTTGTCCATTTTTTTTGTAACTGGCTAA

      AAACTTTATTTCTCTGCCCGCATTAGTCTGGAGAGAGGATGGACGTCATTTTATTCTGAC
1441  -----+-----+-----+-----+-----+-----+-----+ 1500
      TTTGAAATAAAGAGACGGGCGTAATCAGACCTCTCTCCTACCTGCAGTAAATAAGACTG

```

Fig. 8 (cont.)

```

TAAAGTCAGTAAAGAAGCAAACAGATATCTTATTTCTGATCTGGAGCAGCGAAATCCCCG
1501 -----+-----+-----+-----+-----+-----+ 1560
ATTTTCAGTCATTTCTTCGTTTGTCTATAGAATAAAGACTAGACCTCGTCGCTTTAGGGGC

TGTTCCTCGAACAGTCTGAGTTTGAGGCGTTATATCAGGGGCATATTATTCTTATCGCTTC
1561 -----+-----+-----+-----+-----+-----+ 1620
ACAAGAGCTTGTCTAGACTCAAACCTCCGCAATATAGTCCCGTATAATAAGAATAGCGAAG

CCGTTCTTCTGTTGCCGGGAAACTGGCGAAATTTGACTTTACCTGGTTTATTCTGCCAT
1621 -----+-----+-----+-----+-----+-----+ 1680
GGCAAGAAGACAACGGCCCTTTGACCGCTTTAAACTGAAATGGACCAAATAAGGACGGTA

TATAAAATACAGGAGAATATTTATTGAAACCCTTGTGTGTCTGTTTTTTTACAATTATT
1681 -----+-----+-----+-----+-----+-----+ 1740
ATATTTTATGTCCTCTTATAAATAACTTTGGGAACAACACAGACAAAAAATGTTAATAA

TGCATTAATAACCCCCCTTTTTTTTCAGGTGGTTATGGACAAAGTATTAGTGCACAGGGG
1741 -----+-----+-----+-----+-----+-----+ 1800
ACGTAATTATTGGGGGGAAAAAAAGTCCACCAATACCTGTTTCATAATCACGTGTCCCC

ATTTTCAACTCTTAATGTTATTACTGTCGCATTATCTGTTGTGGTGGTGGTTGAGATTAT
1801 -----+-----+-----+-----+-----+-----+ 1860
TAAAGTTGAGAATTACAATAATGACAGCGTAATAGACAACACCACCACAACTCTAATA

ACTCAGCGGTTTAAGAACTTACATTTTGCACATAGTACAAGTCGGATTGATGTTGAGTT
1861 -----+-----+-----+-----+-----+-----+ 1920
TGAGTCGCCAAATTCTTGAATGTAAAAACGTGTATCATGTTTCAGCCTAACTACAAC TCA

GGGTGCCAAACTCTTCCGGCATTACTGGCGCTACCGATCTCTTATTTTGAGAGTCGTCG
1921 -----+-----+-----+-----+-----+-----+ 1980
CCCACGGTTTGAGAAGGCCGTAAATGACCGCGATGGCTAGAGAATAAAACTCTCAGCAGC

TGTTGGTGATACTGTTGCCAGGGTAAGAGAATTAGACCAGATCCGTAATTTTCTGACAGG
1981 -----+-----+-----+-----+-----+-----+ 2040
ACAACCACTATGACAACGGTCCCATTTCTTAACTCTGGTCTAGGCATTTAAAGACTGTCC

ACAGGCATTAACATCTGTTCTGGACTTATTATTTTCATTCATATTTTTTGCGGTAATGTG
2041 -----+-----+-----+-----+-----+-----+ 2100
TGTCCGTAATTGTAGACAAGACCTGAATAATAAAAGTAAGTATAAAAAACGCCATTACAC

```

Fig. 8 (cont.)

HindIII
|

2101 GTATTACAGTCCAAAGCTTACTCTGGTGATCTTATTTTCGCTGCCTTGTTATGCTGCATG
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2160
CATAATGTCAGGTTTCGAATGAGACCACTAGAAATAAAGCGACGGAACAATACGACGTAC

2161 GTCTGTTTTATTAGCCCCATTTTGGCAGCTCGCCTTGATGATAAGTTTTACGGAATGC
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2220
CAGACAAAATAATCGGGGTAAAACGCTGCAGCGGAACCTACTATTCAAAGTGCCTTACG

2221 GGATAATCAATCTTTCCTGGTGAATCAGTCACGGCGATTAACTATAAAAGCTATGGC
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2280
CCTATTAGTTAGAAAGGACCACCTTAGTCAGTGCCGCTAATTGTGATATTTTCGATACCG

PstI
|

2281 AGTCTCACCTCAGATGACGAACATATGGGACAAACAATTGGCAGGATATGTTGCTGCAGG
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2340
TCAGAGTGGAGTCTACTGCTTGATACCCTGTTGTTAACCGTCTATACAACGACGTCC

2341 CTTCAAAGTGACAGTATTAGCAACCATTGGTCAACAAGGAATACAGTTAATAACAAAAGAC
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2400
GAAGTTTCACTGTCATAATCGTTGGTAACCAGTTGTTCTTATGTCAATTATGTTTCTG

2401 TGTTATGATCATCAACCTGTGGTTGGGAGCACACCTGGTTATTTCCGGGGATTAAAGTAT
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2460
ACAATACTAGTAGTTGGACACCAACCCTCGTGTGGACCAATAAAGGCCCTAAATTCATA

2461 TGGTCAGTTAATTGCTTTTAATATGCTTGCTGGTCAGATTGTTGCACCGGTTATTTCGCCT
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2520
ACCAGTCAATTAACGAAAATTATACGAACGACAGTCTAACAACGTGGCCAATAAGCGGA

2521 TGCACAAATCTGGCAGGATTTCCAGCAGGTTGGTATATCAGTTACCCGCCTTGGTGATGT
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2580
ACGTGTTTAGACCGTCCTAAAGGTCTGTCACCATATAGTCAATGGCGGAACCACTACA

2581 GCTTAACTCTCCTGAAAGTTATCATGGGAACTGGCATTACCGGAAATTAATGGTGA
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2640
CGAATTGAGAGGTTGACTTTCAATAGTACCCTTTGACCGTAATGGCCTTTAATTACCACT

2641 TATCACTTTTCGTAATATCCGGTTTCGCTATAAGCCTGACTCTCCGGTTATTTAGATAA
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2700
ATAGTGAAGCATTATAGGCCAAAGCGATATTCGGACTGAGAGGCCAATAAATCTATT

2701 TATCAATCTCAGTATTAAGCAGGGGGAGGTTATTGGTATTGTCGGACGTTCTGGTTCAGG
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2760
ATAGTTAGAGTCATAATTCGTCCCCCTCCAATAACCATAACAGCCTGCAAGACCAAGTCC

Fig. 8 (cont.)

23/30

AAAAAGCACATTAAGTAAATTAATTCAACGTT
2761 -----+-----+-----+----- 2792
TTTTTCGTGTAATTGATTTAATTAAGTTGCAA

Cutting enzymes:

BamHI HindIII NcoI PstI SalI SfiI

Not cutting enzymes:

EcoRI NotI

Fig. 8 (cont.)

PVamyZHLA map

With 11 enzymes: ECORI SPHI PSTI NCOI NHEI NDEI BAMHI HINDIII
SALI SFII NOTI

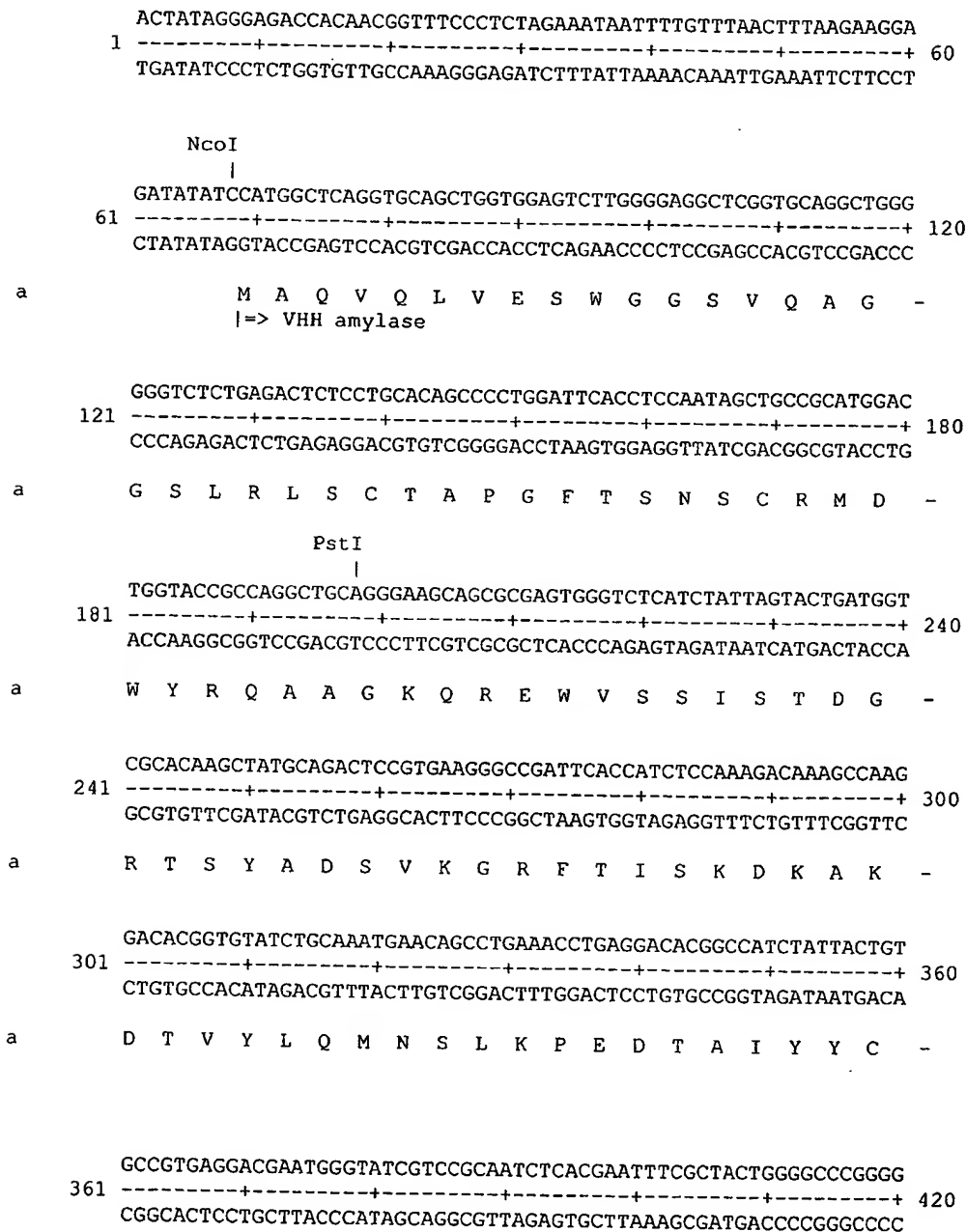


Fig. 9

25/30

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a      A V R T N G Y R P Q S H E F R Y W G P G -

                                     SfiI   SalI
                                     |     |
421  ACCCAGGTCACCGTCTCCTCAACGGCCTCGGGGGCCGCGTCGACGTCCGGCGGTCCGAAG
-----+-----+-----+-----+-----+-----+-----+-----+ 480
      TGGGTCCAGTGGCAGAGGAGTTGCCGGAGCCCCCGGCGCAGCTGCAGGCCGCCAGGCTTC

a      T Q V T V S S T A S G A A S T S G G P K -
                                     |=> Ig hinge

      CCTTCCACTCCGCCCCGGGTCTTCCCGTATGAAACAGCTGGAAGACAAAGTAGAgGAGCTC
481  -----+-----+-----+-----+-----+-----+-----+ 540
      GGAAGGTGAGGCGGGCCAGAGGGCATACTTTGTCGACCTTCTGTTTCATCTTCTCGAG

a      P S T P P G S S R M K Q L E D K V E E L -
                                     |=> Leucine Zipper GCN4

                                     HindIII
                                     |
541  CTTAGCAAGAACTACCATCTAGAAAACGAGGTAGCTCGTCTGAAAAAGCTTGTGGTGAA
-----+-----+-----+-----+-----+-----+-----+ 600
      GAATCGTTCTTGATGGTAGATCTTTTGCTCCATCGAGCAGACTTTTTCGAACAACCACTT

a      L S K N Y H L E N E V A R L K K L V G E -

                                     SalI
                                     |
601  CGTGGTGGTCACCATCACCATCACCATGCGTCGACGCCCGGGGGTGCGCCGGTGCCGTAT
-----+-----+-----+-----+-----+-----+-----+ 660
      GCACCACCACTGGTAGTGGTAGGTACGCAGCTGCGGGCCCCACGCGGCCACGGCATA

a      R G G H H H H H A S T P G G A P V P Y -
      |=> 6xhis tag                                     |=> E-tag

      BamHI
      |
661  CCGGATCCGCTGGAACCGGCCGGGgAAAATtCTCTTGCTAAAAATGTATTATCCGGTGA
-----+-----+-----+-----+-----+-----+-----+ 720
      GGCTAGGCGACCTTGCGCGGCCcTTTTAaGAGAACGATTTTACATAATAGGCCACCT

a      P D P L E P A G E N S L A K N V L S G G -
                                     |=> C-hlyA

      AAAGGTAATGACAAGTTGTACGGCAGTGAGGGAGCAGACCTGCTTGATGGCGGAGAAGGG
721  -----+-----+-----+-----+-----+-----+-----+ 780
      TTTCCATTACTGTTCAACATGCCGTCACTCCCTCGTCTGGACGAACTACCGCCTCTTCCC

a      K G N D K L Y G S E G A D L L D G G E G -

```

Fig. 9 (cont.)

```

AATGATCTTCTGAAAGGTGGATATGGTAATGATATTTATCGTTATCTTTCAGGATATGGC
781 -----+-----+-----+-----+-----+-----+-----+-----+ 840
TTACTAGAAGACTTTCCACCTATACCATTACTATAAATAGCAATAGAAAGTCCTATACCG

a      N D L L K G G Y G N D I Y R Y L S G Y G -

CATCATATTATTGACGATGAAGGGGGGAAAGACGATAAACTCAGTTTAGCTGATATAGAT
841 -----+-----+-----+-----+-----+-----+-----+ 900
GTAGTATAATAACTGCTACTTCCCCCTTTCTGCTATTTGAGTCAAATCGACTATATCTA

a      H H I I D D E G G K D D K L S L A D I D -

TTCCGGGACGTTGCCTTTAAGCGAGAAGGGAATGACCTCATTATGTATAAAGCTGAAGGT
901 -----+-----+-----+-----+-----+-----+-----+ 960
AAGGCCCTGCAACGGAATTGCTCTTCCCTTACTGGAGTAATACATATTTGACTTCCA

a      F R D V A F K R E G N D L I M Y K A E G -

AATGTTCTTTCTATTGGCCACAAAATGGTATTACATTTAAAACTGGTTTGAAAAAGAG
961 -----+-----+-----+-----+-----+-----+-----+ 1020
TTACAAGAAAGATAACCGGTGTTTTTACCATAATGTAATTTTTGACCAAACCTTTTCTC

a      N V L S I G H K N G I T F K N W F E K E -

TCAGATGATCTCTCTAATCATCAGATAGAGCAGATTTTTGATAAAGACGGCAGGGTAATC
1021 -----+-----+-----+-----+-----+-----+-----+ 1080
AGTCTACTAGAGAGATTAGTAGTCTATCTCGTCTAAAACTATTTCTGCCGTCCCATTAG

a      S D D L S N H Q I E Q I F D K D G R V I -

ACACCAGATTCTCTTAAAAAGCATTTGAATATCAGCAGAGTAATAACAAGGTAAGTTAT
1081 -----+-----+-----+-----+-----+-----+-----+ 1140
TGTGGTCTAAGAGAATTTTTTCGTAAACTTATAGTCGTCTCATTATTGTTCCATTCAATA

a      T P D S L K K A F E Y Q Q S N N K V S Y -

GTGTATGGACATGATGCATCAACTTATGGGAGCCAGGACAATCTTAATCCATTAATTAAT
1141 -----+-----+-----+-----+-----+-----+-----+ 1200
CACATACCTGTACTACGTAGTTGAATACCCTCGGTCCTGTTAGAATTAGGTAATTAATTA

a      V Y G H D A S T Y G S Q D N L N P L I N -

```

Fig. 9 (cont.)

PstI

|

1201 GAAATCAGCAAAATCATTTCAGCTGCAGGTAACCTCGATGTTAAGGAGGAAAGATCTGCC
 -----+-----+-----+-----+-----+-----+ 1260
 CTTTAGTCGTTTTAGTAAAGTCGACGTCCATTGAAGCTACAATTCCTCCTTCTAGACGG

a E I S K I I S A A G N F D V K E E R S A -

NdeI

|

1261 GCTTCTTTATTGCAGTTGTCCGGTAATGCCAGTGATTTTTCATATGGACGGAACCTCAATA
 -----+-----+-----+-----+-----+-----+ 1320
 CGAAGAAATAACGTCAACAGGCCATTACGGTCACTAAAAAGTATACCTGCCTTGAGTTAT

a A S L L Q L S G N A S D F S Y G R N S I -

1321 ACTTTGACAGCATCAGCATAATATATTAATTAAATGATAGCAATCTTACTGGGCTGTGC
 -----+-----+-----+-----+-----+-----+ 1380
 TGAACTGTCGTAGTCGTATTATATAATTAATTTACTATCGTTAGAATGACCCGACACG

a T L T A S A * -

1381 CACATAAGATTGCTATTTTTTTGGAGTCATAATGGATTCTTGTCATAAAATTGATTATGG
 -----+-----+-----+-----+-----+-----+ 1440
 GTGTATTCTAACGATAAAAAAACCTCAGTATTACCTAAGAACAGTATTTTAACTAATACC

1441 GTTATACGCCCTGGAGATTTTAGCCCAATACCATAACGTCTCTGTTAACCCGGAAGAAAT
 -----+-----+-----+-----+-----+-----+ 1500
 CAATATGCGGGACCTCTAAATCGGGTTATGGTATTGCAGAGACAATTGGGCCTTCTTTA

1501 TAAACATAGATTTGACACAGACGGGACTGGTCTGGGATTAACGTCATGGTTGCTTGCTGC
 -----+-----+-----+-----+-----+-----+ 1560
 ATTTGTATCTAAACTGTGCTGCCCTGACCAGACCCTAATTCAGTACCAACGAACGACG

1561 GAAATCTTTAGAACTAAAGGTAAAACAGGTAAAAAAAACAATTGACCGATTAACTTTAT
 -----+-----+-----+-----+-----+-----+ 1620
 CTTTAGAAATCTTGATTCCATTTTGTCCATTTTTTTTGTAACTGGCTAATTTGAAATA

1621 TTCTCTGCCCCGATTAGTCTGGAGAGAGGATGGACGTCATTTTATTCTGACTAAAGTCAG
 -----+-----+-----+-----+-----+-----+ 1680
 AAGAGACGGGCGTAATCAGACCTCTCTCCTACCTGCAGTAAAATAAGACTGATTTTCAGTC

1681 TAAAGAAGCAAACAGATATCTTATTTCTGATCTGGAGCAGCGAAATCCCGTGTTCTCGA
 -----+-----+-----+-----+-----+-----+ 1740
 ATTTCTCGTTTGTCTATAGAATAAAGACTAGACCTCGTCGCTTTAGGGGCACAAGAGCT

Fig. 9 (cont.)

```

ACAGTCTGAGTTTGAGGCGTTATATCAGGGGCATATTATTCTTATCGCTTCCC GTTCTTC
1741 -----+-----+-----+-----+-----+-----+ 1800
TGTCAGACTCAAACCTCCGCAATATAGTCCCCGTATAATAAGAATAGCGAAGGGCAAGAAG

TGTTGCCGGGAAACTGGCGAAATTTGACTTTACCTGGTTTATTCCTGCCATTATAAAATA
1801 -----+-----+-----+-----+-----+-----+ 1860
ACAACGGCCCTTTGACCGCTTTAAACTGAAATGGACCAAATAAGGACGGTAATATTTTAT

CAGGAGAATATTTATTGAAACCCCTTGTTGTGTCTGTTTTTTTACAATTATTTGCATTAAT
1861 -----+-----+-----+-----+-----+-----+ 1920
GTCCTCTTATAATAACTTTGGGAACAACACAGACAAAAAATGTTAATAAACGTAATTA

AACCCCCCTTTTTTTTCAGGTGGTTATGGACAAAGTATTAGTGCACAGGGGATTTTCAAC
1921 -----+-----+-----+-----+-----+-----+ 1980
TTGGGGGGAAAAAAGTCCACCAATACCTGTTTCATAATCAGGTGTCCCCTAAAAGTTG

TCTTAATGTTATTACTGTCTGATTATCTGTTGTGGTGGTGGTTTGGAGATTATACTCAGCGG
1981 -----+-----+-----+-----+-----+-----+ 2040
AGAATTACAATAATGACAGCGTAATAGACAACACCACCACAAACTCTAATATGAGTCGCC

TTTAAGAACTTACATTTTTGACATAGTACAAGTCGGATTGATGTTGAGTTGGGTGCCAA
2041 -----+-----+-----+-----+-----+-----+ 2100
AAATTCTTGAATGTAAAACGTGTATCATGTTTCAGCCTAACTACAACCTCAACCCACGGTT

ACTCTTCCGGCATTACTGGCGCTACCGATCTCTTATTTTGAGAGTCGTCGTGTTGGTGA
2101 -----+-----+-----+-----+-----+-----+ 2160
TGAGAAGGCCGTAAATGACCGCGATGGCTAGAGAATAAAACTCTCAGCAGCACCAACCACT

TACTGTTGCCAGGGTAAGAGAATTAGACCAGATCCGTAATTTTCTGACAGGACAGGCATT
2161 -----+-----+-----+-----+-----+-----+ 2220
ATGACAACGGTCCCATTCTCTTAATCTGGTCTAGGCATTAAAAGACTGTCCTGTCCGTAA

AACATCTGTTCTGGACTTATTATTTTCATTCATATTTTTTGCGGTAATGTGGTATTACAG
2221 -----+-----+-----+-----+-----+-----+ 2280
TTGTAGACAAGACCTGAATAATAAAAGTAAGTATAAAAAACGCCATTACACCATAATGTC

HindIII
|
TCCAAAGCTTACTCTGGTGATCTTATTTTCGCTGCCTTGTTATGCTGCATGGTCTGTTTT
2281 -----+-----+-----+-----+-----+-----+ 2340
AGGTTTCGAATGAGACCACTAGAATAAAAGCGACGGAACAATACGACGTACCAGACAAA

TATTAGCCCCATTTTGGCAGCTCGCCTTGATGATAAGTTTTTCACGGAATGCGGATAATCA
2341 -----+-----+-----+-----+-----+-----+ 2400
ATAATCGGGGTAAAACGCTGCAGCGGAACACTATTCAAAGTGCCTTACGCCTATTAGT

```

Fig. 9 (cont.)

```

ATCTTTCCTGGTGAATCAGTCACGGCGATTAACTATAAAAGCTATGGCAGTCTCACC
2401 -----+-----+-----+-----+-----+-----+ 2460
TAGAAAGGACCACCTTAGTCAGTGCCGCTAATTGTGATATTTTCGATACCGTCAGAGTGG

                NdeI                      PstI
                |                        |
TCAGATGACGAACATATGGGACAAACAATTGGCAGGATATGTTGCTGCAGGCTTCAAAGT
2461 -----+-----+-----+-----+-----+-----+ 2520
AGTCTACTGCTTGTATACCTGTTTGTAAACCGTCTATACAACGACGTCCGAAGTTTCA

GACAGTATTAGCAACCATTGGTCAACAAGGAATACAGTTAATACAAAAGACTGTTATGAT
2521 -----+-----+-----+-----+-----+-----+ 2580
CTGTCATAATCGTTGGTAACCAAGTTGTTCCCTATGTCAATTATGTTTCTGACAATACTA

CATCAACCTGTGGTGGGAGCACACCTGGTTATTTCCGGGGATTAAAGTATTGGTCAGTT
2581 -----+-----+-----+-----+-----+-----+ 2640
GTAGTTGGACACCAACCCTCGTGTGGACCAATAAAGGCCCTAAATTCATAACCAAGTCAA

AATTGCTTTTAAATATGCTTGCTGGTCAGATTGTTGCACCGGTTATTCGCCTTGCACAAAT
2641 -----+-----+-----+-----+-----+-----+ 2700
TTAACGAAAATTATACGAACGACCAGTCTAACAACGTGGCCAATAAGCGGAACGTGTTA

CTGGCAGGATTTCCAGCAGGTTGGTATATCAGTTACCCGCCCTTGGTGATGTGCTTAACTC
2701 -----+-----+-----+-----+-----+-----+ 2760
GACCGTCTAAAGGTCGTCCAACCATATAGTCAATGGGCGGAACCACTACACGAATTGAG

TCCAACTGAAAGTTATCATGGGAAACTGGCATTACCGGAAATTAATGGTGATATCACTTT
2761 -----+-----+-----+-----+-----+-----+ 2820
AGGTTGACTTTCAATAGTACCCTTTGACCGTAATGGCCTTTAATTACCACTATAGTGAAA

TCGTAATATCCGGTTTCGCTATAAGCCTGACTCTCCGGTTATTTTAGATAATATCAATCT
2821 -----+-----+-----+-----+-----+-----+ 2880
AGCATTATAGGCCAAAGCGATATTCGGACTGAGAGGCCAATAAAATCTATTATAGTTAGA

CAGTATTAAGCAGGGGGAGGTTATTGGTATTGTGCGACGTTCTGGTTCAGGAAAAAGCAC
2881 -----+-----+-----+-----+-----+-----+ 2940
GTCATAATTGTCCTCCCTCCAATAACCATAACAGCCTGCAAGACCAAGTCCTTTTTCGTG

ATTAACATAAATTAATTCAACGTT
2941 -----+-----+-----+-----+-----+ 2963
TAATTGATTTAATTAAGTTGCAA

```

Fig. 9 (cont.)

30/30

Cutting enzymes:

BamHI	HindIII	NcoI	NdeI	PstI	SalI	SfiI
-------	---------	------	------	------	------	------

Not cutting enzymes:

EcoRI	NheI	NotI	SphI
-------	------	------	------

Fig. 9 (cont.)

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